

Estimation of Genetic Variability Parameters in Different Genotypes of Rice (*Oryza sativa* L.)

Deepak Meena^{*1}, Manoj Kumar², Sandhya², R.K. Meena³ and J.K. Meena¹

¹Department of Genetics and Plant Breeding, Rajasthan College of Agriculture, MPUAT, Udaipur, Rajasthan, India

²Agricultural Research Station Umedganj, AU Kota, Rajasthan, India

³Department of Agronomy, College of Agriculture, Umedganj, AU Kota, Rajasthan, India

(Received 18 October, 2022; Accepted 17 December, 2022)

ABSTRACT

Studies on different genetic variability parameters *viz.*, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance were carried out with 25 genotypes of Rice (*Oryza Sativa* L.) for 10 characters at Agriculture Research Station, Umedganj, Kota, Rajasthan. The analysis of variance indicated the existence of significant differences among genotypes for all the characters studied. High GCV and PCV values were observed for grain yield per plant, number of productive tillers per plant, number of grains per panicle and 1000-grain indicating the presence of good amount of genetic variability for these characters so, direct selection for these characters would be effective. The characters *viz.*, number of productive tillers per plant and grain yield per plant exhibited high heritability coupled with high genetic advance indicating the involvement of additive gene action in the inheritance of these traits hence simple selection would be rewarding.

Key words : Genetic advance, Genetic variability, Heritability, rice

Introduction

Rice (*Oryza sativa* L.) is the global's most extensive staple cereal crop after wheat. It is an annual, self-pollinated, C₃ crop plant with chromosome number 2n=2x=24. It belongs to the family Poaceae. The rice genus consists of 24 species, in which 22 are wild and two are cultivated, *i.e.* *O. sativa* and *O. glaberrima*. It is originated from South-eastern Asia. Rice is the primary source of food and calories for about half of the mankind (Khush, 2005) providing staple food for more than 60 per cent of the global population, about 75 per cent of the calorie and 55 per cent of the protein intake in their average daily diet. Rice bran oil is used as medicine as well as cooking oil and its straw and bran are important

animal feed in many countries. Rice is a short day crop, needs a hot humid climate with average temperature 21 to 37 °C, throughout the life cycle of crop. It is grown under variable conditions and production systems. It is the only cereal crop that can grow for long periods of time in standing water to rainfed upland conditions with short span of time. Asia is known as a 'rice bowl' of the world. Approximately 90 per cent of the world's rice is grown in the Asian continent. India ranks first in area 45.06 million hectare and second in the production 122.27 million tonnes with a productivity of 2713 kg/ha. (Anonymous, 2021-22). The success of any crop improvement programme is highly dependent on the efficient manipulation of the genetic variability present in the germplasm and the selection of geno-

types with all possible desirable yield and quality contributing traits. Genotypic and different components of variance, heritability and genetic advance are always considered as a parameter for identification of genotypes having broad genetic variability and characters with high heritability to execute effective selection.

Materials and Methods

The experimental materials for the present study consisted of 25 rice genotypes which were collected from Agriculture Research Station, Ummedganj, Kota, Rajasthan. All the 25 genotypes were sown in nursery on 20 June, 2019 and healthy seedling of 24 days old were transplanted in randomized block design with three replications on 14 July, 2019. Each genotype transplanted in plot of 10m² having ten rows of five meter in length. Row to row and plant to plant distance was maintained 20 cm. and 10 cm. respectively. Observations were recorded on ten randomly selected plants for 10 quantitative characters such as days to 50 per cent flowering, days to maturity, plant height (cm), numbers of productive tillers per plant, panicle length (cm), 1000-grain weight (g), numbers of grains per panicle, amylose content per cent, protein content per cent and grain yield per plant (g). The data collected for each character on individual plant basis for ten randomly selected plants were analyzed. The coefficient of phenotypic and genotypic variation was calculated by using the formula suggested by Burton (1952). Heritability in broad sense (H_{bs}) was calculated according to the following formula suggested by Burton and De Vane (1953). The genetic advance (G.A.) as percentage of mean was calculated by using the formula suggested by Johnson *et al.* (1955).

Results and Discussion

The results of the analysis of variance presented (Table 1) revealed that significant difference among 25 genotypes of rice for ten characters like days to 50 per cent flowering, days to maturity, number of productive tillers panicle per plant, plant height, panicle length, number of grains per panicle, 1000-grains weight, amylose content and protein content which suggested that the materials selected for the study might be of diverse in origin or developed from diverse crosses. Yield and its attributing traits observed in the base population could be utilized to

improve this crop by using simple breeding methods. A wide range of variability for various traits has been observed earlier by Sahu *et al.* (2017), Kishor *et al.* (2018), Mamta *et al.* (2018), Meena *et al.* (2018), Monalisha *et al.* (2018), Kumari *et al.* (2019) and Manjunatha and Kumara (2019).

Genetic improvements through conventional breeding approaches depend mainly on the availability of the diverse germplasm and the amount of genetic variability present in the population for the desired characters. The genotypic coefficient of variation measures the range of variability available in the crop and also enables a breeder to compare the amount of variability present among different characters. The phenotypic expression of the character is the result of interaction between genotype and environment. Hence, the total variance should be partitioned into heritable and non heritable components

Table 1. Analysis of variance for yield and its attributing traits in rice genotypes

Source of variation	Degree of freedom	Mean sum of square									
		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of productive tillers per plant	Panicle length (cm)	Number of grains per panicle	1000-grain weight (g)	Amylose content (%)	Protein content (%)	Grain yield per plant (g)
Replication	2	1.69	4.17	23.69	0.33	0.59	47.61	0.52	0.03	0.05	4.73
Genotypes	24	202.71**	227.04**	121.36**	9.91**	5.12**	930.51**	19.45**	4.89**	1.25**	38.56**
Error	48	1.25	2.02	15.62	0.49	0.21	214.89	0.19	0.20	0.05	1.59

*, ** = Significant at 5 and 1 per cent level, respectively.

to assess the true breeding nature of the particular trait under study. The heritable portion of the variation can be ascertained by studying the components of variation such as GCV, PCV, heritability and predicted genetic advance. In present study, as per (Table 2) the results indicated that the estimates of PCV were higher than their corresponding GCV for all the traits studied which indicated effect of environment on the expression of characters. The characters like grain yield per plant, number of productive tillers per plant, number of grains per panicle and 1000-grain weight showed higher estimates of GCV and PCV, indicating the presence of good amount of variation among the genotypes for these characters. Therefore, simple selection of these characters would be effective because the response of selection is directly proportional to variability present in the experimental material. These findings are in accordance with earlier findings of Tuhina *et al.* (2015), Anis *et al.* (2016), Sala *et al.* (2016), Meena *et al.* (2018) and Ismaeel (2018). The characters like panicle length, amylose content, plant height having low estimates of GCV and PCV indicating the low range of variation found in these characters in the present experimental material, thus offers little scope for further improvement of these characters. Similar kinds of findings were earlier reported by Abdul *et al.* (2011), Pathak *et al.* (2016), and Singh *et al.* (2017).

The coefficient of variation alone is not sufficient to determine the amount of heritable variability from one generation to the next generation. The heritable portion of variation is thus required to be estimated with the help of heritable estimates (Burton, 1952). The high heritability was recorded for most of the character except number of grains per panicle. Days to 50 per cent flowering exhibited

highest heritability followed by days to maturity, 1000-grain weight, amylose content, grain yield per plant, panicle length, protein content, number of productive tillers per plant and protein content. This indicated that selection of these traits would be more effective as compared to others. Similar findings were reported earlier by Singh *et al.* (2017), Bagudam *et al.* (2018), Mamta *et al.* (2018), Kumari *et al.* (2019) and Tiwari *et al.* (2019).

The heritability estimates alone do not provide authentic information about the gene governing the expression of a particular character and this do not provide the information of the amount of genetic progress that would result from the selection of best individuals. Johanson *et al.* (1955) had pointed about that the heritability estimates along with genetic advance as percent of mean were more useful than heritability estimates alone in predicting the response to selection. In the present investigation genetic advance as per cent of mean was highest for grain yield per plant and number of productive tillers per plant and 1000-grain weight, whereas it was moderate for days to 50 per cent flowering, protein content, number of grains per panicle, days to maturity, amylose content and it was low for plant height and panicle length.

Heritability and genetic advance as per cent of mean are two complementary concepts. Thus, heritability values may be used to estimate the genetic advance through selection for predicting the utility and value of selection. In the present investigation, High heritability along with high genetic advance as per cent of mean was observed for grain yield per plant, number of productive tillers per plant and 1000-grain weight indicating the involvement of additive gene action in the inheritance of these traits

Table 2. Genetic variability parameters for yield and its attributing traits in rice genotypes.

Sr. No.	Characters	Range	Mean	GCV (%)	PCV (%)	Heritability % (b.s)	Genetic advance	Gen. Adv as % of mean
1.	Days to 50% flowering	78.67-104.00	94.09	8.71	8.79	98.17	16.73	17.78
2.	Days to maturity	112.67-140.00	129.25	6.70	6.79	97.38	17.60	13.62
3.	Plant height (cm)	95.00-117.33	108.03	5.50	6.60	69.29	10.18	9.42
4.	Number of productive tillers per plant	5.33-11.00	8.03	22.09	23.73	86.60	3.39	42.35
5.	Panicle length (cm)	25.23-29.83	27.59	4.64	4.93	88.47	2.48	8.98
6.	Number of grains per panicle	133.67-199.00	164.25	9.40	12.96	52.61	23.08	14.05
7.	1000-grain weight (g)	21.70-30.33	25.61	9.89	10.04	97.07	5.15	20.08
8.	Amylose content (%)	22.33-26.80	23.90	5.23	5.55	88.85	2.43	10.16
9.	Protein content (%)	6.86-9.37	8.06	7.82	8.33	88.18	1.22	15.13
10.	Grain yield per plant (g)	8.87-19.03	13.73	25.56	27.16	88.58	6.81	49.55

hence simple selection would be rewarding.

References

- Abdul, F.R., Ramya, K.T., Chikkalingaiah, Ajay, B.C., Gireesh, C. and Kulkarni, R.S. 2011. Genetic variability, correlation and path coefficient analysis studies in rice (*Oryza sativa* L.) under alkaline soil condition. *Electronic Journal of Plant Breeding*. 2 (4): 531-537.
- Anis, G., Sabagh, E.L., Ayman, G., Abdelfatah, E.I. and Rewainy, I. 2016. Evaluation of promising lines in rice (*Oryza sativa* L.) to agronomic and genetic performance under Egyptian conditions. *International Journal of Agronomy and Agricultural Research*. 8 (3): 52-57.
- Anonymous, 2021-22. Annual Report, Department of Agriculture and Farmers Welfare Ministry of Agriculture and Farmers Welfare Government of India Krishi Bhawan, New Delhi-110 001.
- Bagudam, R., Eswari, K.B., Badri, J. and Rao, P.R. 2018. Research Note Variability, heritability and genetic advance for yield and its component traits in NPT core set of rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*. 9 (4): 1545-1551.
- Burton, G.W. 1952. Quantitative inheritance in grasses. *Proceedings 6th international grassland congress Journal*. 1: 227-283.
- Burton, G.W. and Devane, E.H. 1953. Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. *Agronomy Journal*. 45: 478-481.
- Ismaeel, M. 2018. Assessment of genetic variability, heterosis and heritability for morphological parameters in rice. *Pure and Applied Biology*. 8 (1): 160-168.
- Johnson, H.W., Robinson, H.E. and Comstock, R.E. 1955. Estimation of genetic and environmental variability in soybean. *Agronomy Journal*. 47(7): 314-318.
- Khush, G.S. 2005. what it will take to feed 5.0 billion rice consumers in 2030. *Plant Molecular Biology*. 59 (1): 1-6.
- Kishor, C., K., Anil, K.P., Awadhesh, K. and Vinod, 2018. Character association and path analysis for yield components in traditional rice (*Oryza sativa* L.) genotypes. *International Journal of Current Microbiology and Applied Sciences*. 7(3): 283-291.
- Kumari, N., Kumar, R. and Kumar, A. 2019. Genetic Variability and Association of Traits in Mutant Lines of Rice (*Oryza sativa* L.) for Submergence Tolerance. *Journal of Applied Science and Technology*. 33 (2): 1-7.
- Kumari, N., Kumar, R. and Kumar, A. 2019. Genetic Variability and Association of Traits in Mutant Lines of Rice (*Oryza sativa* L.) for Submergence Tolerance. *Journal of Applied Science and Technology*. 33 (2): 1-7.
- Mamata, K., Rajana, M.P. and Savita, S.K. 2018. Assessment of genetic parameters for yield and its related traits in F₂ populations involving traditional varieties of rice (*Oryza sativa* L.). *International Journal of Current Microbiology and Applied Sciences*. 7 (1): 2210-2217.
- Manjunatha, B. and Kumara, B.N. 2019. Genetic variability analysis for quantitative traits in rice (*Oryza sativa* L.). *Journal of Experimental Agriculture International*. 30 (4): 1-4.
- Meena, S., Kumar, R., Maurya, V., Bisen, P., Loitongbam, B., Rathi, S.R. and Singh, P.K. 2018. Estimation of variability parameters, correlation and path coefficient for yield and yield associated traits in rice (*Oryza sativa* L.). *International Journal of Agriculture, Environment and Biotechnology, IJAEB*. 867-873.
- Monalisha, P. and Das, S.R. 2018. Genetic variability, correlation and path analysis in hybrid rice. *International Journal of Agriculture Sciences*. 10 (14): 6691-6693.
- Pathak, K., Verma, H., Sarma, R. and Samindra, B. 2016. Variability in grain quality characters of local winter (sali) rice of assam, india. *Indian Journal of Plant Genetic Resources*. 29 (1) : 22-31.
- Sahu, P.K., Sharma, D., Mondal, S., Kumar, V., Singh, S., Baghel, S., Tiwari, A., Vishwakarma, G. and Das, B.K. 2017. Genetic variability for grain quality traits in indigenous rice landraces of Chhattisgarh, India. *Journal of Experimental Biology and Agricultural Sciences*. 5 (4): 439-455.
- Sala, M. and Shanthi, P. (2016). Variability, heritability and genetic advance studies in F₂ population of rice (*Oryza sativa* L.). *International Journal of Forestry and Crop Improvement*. 7(1): 57-60.
- Singh, S.K., Singh, C. and Mandlal, G.M. 2017. Assessment of genetic variability for yield and its component characters in rice (*Oryza sativa* L.). *Research in Plant Biology*. 1(4): 89-91.
- Tiwari, D.N., Tripathi, S.R., Tripathi, M.P., Khatri, N. and Bastola, B.R. 2019. Genetic variability and correlation coefficients of major traits in early maturing rice under rainfed low land environments of Nepal. *Advances in Agriculture*. 5975901: 9.
- Tuhina, K.M., Hanafi, M.M., Yusop, M.R., Wong, M.Y., Salleh, F.M. and Ferdous, J. 2015. Genetic variation, heritability, and diversity analysis of upland rice (*Oryza sativa* L) Genotypes Based on Quantitative Traits. *Bio Med Research International*. 290861: 7.
- Verma, D.D., Hota, M., Randhawa, G.J., Bhalla, S., Chalam, V.C. and Tyagi, V. 2006. Documents on biology of Rice (*Oryza sativa* L.) in India. National bureau of Plant Genetic Resources. Indian council of Agriculture Research, New Delhi. *Alpha Lithographics Inc*. 1-88.